It is not believed that extensions of time or fees for net addition of claims are required beyond those that may otherwise be provided for in documents accompanying this paper. However, if additional extensions of time are necessary to prevent abandonment of this application, then such extensions of time are hereby petitioned under 37 C.F.R. § 1.136(a), and any fees required therefor (including fees for net addition of claims) are hereby authorized to be charged to our Deposit Account No. 19-0036.

Amendments

In the Claims:

Please substitute the following claim 95 for the pending claim 95:

95.   (thrice amended)   An isolated polynucleotide encoding a polypeptide comprising an amino acid sequence at least 95% identical to amino acids 1 to 260 of SEQ ID NO:42;

wherein % identity is determined with parameters that calculate % identity over the full length of amino acids 1 to 260 of SEQ ID NO:42 and that allow gaps of up to 5% of the total number of residues in amino acids 1 to 260 of SEQ ID NO:42; and

wherein said polypeptide forms a $GABA_A$ receptor complex with α- and β- $GABA_A$ receptor subunits.

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Please substitute the following claim 98 for the pending claim 98:

98.   (thrice amended) An isolated polynucleotide encoding a polypeptide comprising an amino acid sequence at least 95% identical to amino acids 1 to 488 of SEQ ID NO:42;

wherein % identity is determined with parameters that calculate % identity over the full length of amino acids 1 to 488 of SEQ ID NO:42 and that allow gaps of up to 5% of the total number of residues in amino acids 1 to 488 of SEQ ID NO:42; and

wherein said polypeptide forms a $GABA_A$ receptor complex with α- and β- $GABA_A$ receptor subunits.

Please substitute the following claim 101 for the pending claim 101:

101.   (thrice amended) An isolated polynucleotide comprising a nucleotide sequence encoding a polypeptide comprising an amino acid sequence at least 95% identical to amino acids -17 to 488 of SEQ ID NO:42;

wherein % identity is determined with parameters that calculate % identity over the full length of amino acids -17 to 488 of SEQ ID NO:42 and that allow gaps of up to 5% of the total number of residues in amino acids -17 to 488 of SEQ ID NO:42; and

wherein said polypeptide forms a $GABA_A$ receptor complex with α- and β- $GABA_A$ receptor subunits.

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Please substitute the following claim 104 for the pending claim 104:

104. (thrice amended) An isolated polynucleotide comprising a nucleotide sequence encoding a polypeptide comprising an amino acid sequence at least 95% identical to amino acids -18 to 488 of SEQ ID NO:42;

wherein % identity is determined with parameters that calculate % identity over the full length of amino acids -18 to 488 of SEQ ID NO:42 and that allow gaps of up to 5% of the total number of residues in amino acids -18 to 488 of SEQ ID NO:42; and

wherein said polypeptide forms a GABA$_A$ receptor complex with α- and β- GABA$_A$ receptor subunits.

Please substitute the following claim 115 for the pending claim 115:

115. (thrice amended) An isolated polynucleotide encoding a polypeptide comprising an amino acid sequence at least 95% identical to the mature amino acid sequence encoded by the cDNA clone in ATCC Deposit No. 209642,

wherein % identity is determined with parameters that calculate % identity over the full length of the mature amino acid sequence encoded by the cDNA clone in ATCC Deposit No. 209642 and that allow gaps of up to 5% of the total number of residues of the mature amino acid sequence encoded by the cDNA clone in ATCC Deposit No. 209642; and

wherein said polypeptide forms a GABA$_A$ receptor complex with α- and β- GABA$_A$ receptor subunits.

Please substitute the following claim 117 for the pending claim 117:

117. (thrice amended) An isolated polynucleotide encoding a polypeptide comprising an amino acid sequence at least 95% identical to the complete amino acid sequence encoded by the cDNA clone in ATCC Deposit No. 209642;

wherein % identity is determined with parameters that calculate % identity over the full length of the complete amino acid sequence encoded by the cDNA clone in ATCC Deposit No. 209642 and that allow gaps of up to 5% of the total number of residues of the complete amino acid sequence encoded by the cDNA clone in ATCC Deposit No. 209642; and

wherein said polypeptide forms a GABA$_A$ receptor complex with α- and β- GABA$_A$ receptor subunits.

Please substitute the following claim 118 for the pending claim 118:

118. (once amended) The isolated polynucleotide of claim 117, wherein the polypeptide comprises the complete amino acid sequence encoded by the cDNA clone in ATCC Deposit No. 209642.